

PCT09

RAW SEQUENCE LISTING
 PATENT APPLICATION: US/09/786,024

DATE: 08/01/2001
 TIME: 18:18:38

Input Set : A:\09786024SeqList.txt
 Output Set: N:\CRF3\08012001\I786024.raw

ENTERED

```

2 <110> APPLICANT: Yu, Long
3     Fu, Qiang
4     Zhao, Yong
5     Zhang, Honglai
6     Bi, Anding
8 <120> TITLE OF INVENTION: A NOVEL HUMAN LYSOZYME GENE, ITS ENCODED
9     POLYPEPTIDE AND THE METHOD FOR PREPARING THEM
12 <130> FILE REFERENCE: A34054-PCT-USA 072975.0110
14 <140> CURRENT APPLICATION NUMBER: 09/786,024
15 <141> CURRENT FILING DATE: 1999-08-30
17 <150> PRIOR APPLICATION NUMBER: CN 98111041.X
18 <151> PRIOR FILING DATE: 1998-08-31
20 <160> NUMBER OF SEQ ID NOS: 12
22 <170> SOFTWARE: FastSEQ for Windows Version 4.0
24 <210> SEQ ID NO: 1
25 <211> LENGTH: 23
26 <212> TYPE: DNA
27 <213> ORGANISM: Artificial Sequence
29 <220> FEATURE:
30 <223> OTHER INFORMATION: Oligonucleotide primer
32 <400> SEQUENCE: 1
33 agagtgtggtg tggtccact ctg                                23
35 <210> SEQ ID NO: 2
36 <211> LENGTH: 23
37 <212> TYPE: DNA
38 <213> ORGANISM: Artificial Sequence
40 <220> FEATURE:
41 <223> OTHER INFORMATION: Oligonucleotide primer
43 <400> SEQUENCE: 2
44 tgctgtgcat ggttccgtcc atc                                23
46 <210> SEQ ID NO: 3
47 <211> LENGTH: 544
48 <212> TYPE: DNA
49 <213> ORGANISM: Human
51 <220> FEATURE:
52 <221> NAME/KEY: CDS
53 <222> LOCATION: (81)...(521)
54 <223> OTHER INFORMATION: Lysozyme LYCH3
56 <400> SEQUENCE: 3
57 agagtgtggtg tggtccact ctgccgccgc atagaagcca ggagcagggc tctcagaagg 60
58 cgggtggtgcc agctgggac atg ttg ttg gcc ctg gtc tgt ctg ctc agc tgc 113
59                               Met Leu Leu Ala Leu Val Cys Leu Leu Ser Cys
60                               1           5           10
62 ctg cta ccc tcc agt gag gcc aag ctc tac ggt cgt tgt gaa ctg gcc    161
63 Leu Leu Pro Ser Ser Glu Ala Lys Leu Tyr Gly Arg Cys Glu Leu Ala
64                               15           20           25
66 aga gtg cta cat gac ttc ggg ctg gac gga tac cgg gga tac agc ctg    209

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67 Arg Val Leu His Asp Phe Gly Leu Asp Gly Tyr Arg Gly Tyr Ser Leu
68          30          35          40
70 gct gac tgg gtc tgc ctt gct tat ttc aca agc ggt ttc aac gca gct 257
71 Ala Asp Trp Val Cys Leu Ala Tyr Phe Thr Ser Gly Phe Asn Ala Ala
72          45          50          55
74 gct ttg gac tac gag gct gat ggg agc acc aac aac ggg atc ttc cag 305
75 Ala Leu Asp Tyr Glu Ala Asp Gly Ser Thr Asn Asn Gly Ile Phe Gln
76 60          65          70          75
78 atc aac agc cgg agg tgg tgc agc aac ctc acc ccg aac gtc ccc aac 353
79 Ile Asn Ser Arg Arg Trp Cys Ser Asn Leu Thr Pro Asn Val Pro Asn
80          80          85          90
82 gtg tgc cgg atg tac tgc tca gat ttg ttg aat cct aat ctc aag gat 401
83 Val Cys Arg Met Tyr Cys Ser Asp Leu Leu Asn Pro Asn Leu Lys Asp
84          95          100          105
86 acc gtt atc tgt gcc atg aag ata acc caa gag cct cag ggt ctg ggt 449
87 Thr Val Ile Cys Ala Met Lys Ile Thr Gln Glu Pro Gln Gly Leu Gly
88          110          115          120
90 tac tgg gag gcc tgg agg cat cac tgc cag gga aaa gac ctc act gaa 497
91 Tyr Trp Glu Ala Trp Arg His His Cys Gln Gly Lys Asp Leu Thr Glu
92          125          130          135
94 tgg gtg gat ggc tgt gac ttc tag gatggacgga accatgcaca gca 544
95 Trp Val Asp Gly Cys Asp Phe *
96 140          145
99 <210> SEQ ID NO: 4
100 <211> LENGTH: 146
101 <212> TYPE: PRT
102 <213> ORGANISM: Human
104 <400> SEQUENCE: 4
105 Met Leu Leu Ala Leu Val Cys Leu Leu Ser Cys Leu Leu Pro Ser Ser
106 1          5          10          15
107 Glu Ala Lys Leu Tyr Gly Arg Cys Glu Leu Ala Arg Val Leu His Asp
108          20          25          30
109 Phe Gly Leu Asp Gly Tyr Arg Gly Tyr Ser Leu Ala Asp Trp Val Cys
110          35          40          45
111 Leu Ala Tyr Phe Thr Ser Gly Phe Asn Ala Ala Ala Leu Asp Tyr Glu
112          50          55          60
113 Ala Asp Gly Ser Thr Asn Asn Gly Ile Phe Gln Ile Asn Ser Arg Arg
114 65          70          75          80
115 Trp Cys Ser Asn Leu Thr Pro Asn Val Pro Asn Val Cys Arg Met Tyr
116          85          90          95
117 Cys Ser Asp Leu Leu Asn Pro Asn Leu Lys Asp Thr Val Ile Cys Ala
118          100          105          110
119 Met Lys Ile Thr Gln Glu Pro Gln Gly Leu Gly Tyr Trp Glu Ala Trp
120          115          120          125
121 Arg His His Cys Gln Gly Lys Asp Leu Thr Glu Trp Val Asp Gly Cys
122          130          135          140
123 Asp Phe
124 145
127 <210> SEQ ID NO: 5

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128 <211> LENGTH: 29
129 <212> TYPE: DNA
130 <213> ORGANISM: Artificial Sequence
132 <220> FEATURE:
133 <223> OTHER INFORMATION: Oligonucleotide primer
135 <400> SEQUENCE: 5
136 tctcgatcc atgttggttg ccctggtct 29
138 <210> SEQ ID NO: 6
139 <211> LENGTH: 29
140 <212> TYPE: DNA
141 <213> ORGANISM: Artificial Sequence
143 <220> FEATURE:
144 <223> OTHER INFORMATION: Oligonucleotide primer
146 <400> SEQUENCE: 6
147 ccttgatcgac ctagaagtca cagccatcc 29
149 <210> SEQ ID NO: 7
150 <211> LENGTH: 29
151 <212> TYPE: DNA
152 <213> ORGANISM: Artificial Sequence
154 <220> FEATURE:
155 <223> OTHER INFORMATION: Oligonucleotide primer
157 <400> SEQUENCE: 7
158 tctcaagctt atgttggttg ccctggtct 29
160 <210> SEQ ID NO: 8
161 <211> LENGTH: 29
162 <212> TYPE: DNA
163 <213> ORGANISM: Artificial Sequence
165 <220> FEATURE:
166 <223> OTHER INFORMATION: Oligonucleotide primer
168 <400> SEQUENCE: 8
169 ccttgatcc ctagaagtca cagccatcc 29
171 <210> SEQ ID NO: 9
172 <211> LENGTH: 27
173 <212> TYPE: DNA
174 <213> ORGANISM: Artificial Sequence
176 <220> FEATURE:
177 <223> OTHER INFORMATION: Oligonucleotide primer
179 <400> SEQUENCE: 9
180 tctcaagctt aagctctacg gtcgttg 27
182 <210> SEQ ID NO: 10
183 <211> LENGTH: 19
184 <212> TYPE: PRT
185 <213> ORGANISM: Artificial Sequence
187 <220> FEATURE:
188 <223> OTHER INFORMATION: Signature sequence of lysozyme and
189 alpha-lactoalbumin
191 <221> NAME/KEY: VARIANT
192 <222> LOCATION: (2)...(4)
193 <223> OTHER INFORMATION: Any amino acid

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195 <221> NAME/KEY: VARIANT
 196 <222> LOCATION: (6)...(7)
 197 <223> OTHER INFORMATION: Any amino acid
 199 <221> NAME/KEY: VARIANT
 200 <222> LOCATION: (8)...(8)
 201 <223> OTHER INFORMATION: Leucine, methionine or phenylalanine
 203 <221> NAME/KEY: VARIANT
 204 <222> LOCATION: (9)...(11)
 205 <223> OTHER INFORMATION: Any amino acid
 207 <221> NAME/KEY: VARIANT
 208 <222> LOCATION: (12)...(12)
 209 <223> OTHER INFORMATION: Aspartate, glutamate or asparagine
 211 <221> NAME/KEY: VARIANT
 212 <222> LOCATION: (13)...(13)
 213 <223> OTHER INFORMATION: Leucine or isoleucine
 215 <221> NAME/KEY: VARIANT
 216 <222> LOCATION: (14)...(18)
 217 <223> OTHER INFORMATION: Any amino acid
 219 <400> SEQUENCE: 10
 220 Cys Xaa Xaa Xaa Cys Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa
 221 1 5 10 15
 222 Xaa Xaa Cys
 226 <210> SEQ ID NO: 11
 227 <211> LENGTH: 148
 228 <212> TYPE: PRT
 229 <213> ORGANISM: Trachypithecus francoisi
 231 <400> SEQUENCE: 11
 232 Met Arg Ala Leu Ile Ile Leu Gly Leu Val Leu Leu Ser Val Thr Val
 233 1 5 10 15
 234 Gln Gly Lys Ile Phe Glu Arg Cys Glu Leu Ala Arg Thr Leu Lys Lys
 235 20 25 30
 236 Leu Gly Leu Asp Gly Tyr Lys Gly Val Ser Leu Ala Asn Trp Val Cys
 237 35 40 45
 238 Leu Ala Lys Trp Glu Ser Gly Tyr Asn Thr Glu Ala Thr Asn Tyr Asn
 239 50 55 60
 240 Pro Gly Asp Glu Ser Thr Asp Tyr Gly Ile Phe Gln Ile Asn Ser Arg
 241 65 70 75 80
 242 Tyr Trp Cys Asn Asn Gly Lys Thr Pro Gly Ala Val Asp Ala Cys His
 243 85 90 95
 244 Ile Ser Cys Ser Ala Leu Leu Gln Asn Asn Ile Ala Asp Ala Val Ala
 245 100 105 110
 246 Cys Ala Lys Arg Val Val Ser Asp Pro Gln Gly Ile Arg Ala Trp Val
 247 115 120 125
 248 Ala Trp Arg Asn His Cys Gln Asn Lys Asp Val Ser Gln Tyr Val Lys
 249 130 135 140
 250 Gly Cys Gly Val
 251 145
 254 <210> SEQ ID NO: 12
 255 <211> LENGTH: 147

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256 <212> TYPE: PRT

257 <213> ORGANISM: Ring-necked pheasant

259 <400> SEQUENCE: 12

260 Met Arg Ser Leu Leu Ile Leu Val Leu Cys Phe Leu Pro Leu Ala Ala

261 1 5 10 15

262 Pro Gly Lys Val Tyr Gly Arg Cys Glu Leu Ala Ala Ala Met Lys Arg

263 20 25 30

264 Met Gly Leu Asp Asn Tyr Arg Gly Tyr Ser Leu Gly Asn Trp Val Cys

265 35 40 45

266 Ala Ala Lys Phe Glu Ser Asn Phe Asn Thr Gly Ala Thr Asn Arg Asn

267 50 55 60

268 Thr Asp Gly Ser Thr Asp Tyr Gly Ile Leu Gln Ile Asn Ser Arg Trp

269 65 70 75 80

270 Trp Cys Asn Asp Gly Arg Thr Pro Gly Ser Lys Asn Leu Cys His Ile

271 85 90 95

272 Pro Cys Ser Ala Leu Leu Ser Ser Asp Ile Thr Ala Ser Val Asn Cys

273 100 105 110

274 Ala Lys Lys Ile Val Ser Asp Gly Asn Gly Met Asn Ala Trp Val Ala

275 115 120 125

276 Trp Arg Lys His Cys Lys Gly Thr Asp Val Asn Val Trp Ile Arg Gly

277 130 135 140

278 Cys Arg Leu

279 145

VERIFICATION SUMMARY

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L:220 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:10

L:222 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:10